the matchAhead procedure

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The matchAhead procedure, from end-to-end, takes a hierarchical dataset $\mathcal{D}$ of schools and students and returns a set of matching distances between every treatment and control school in that dataset. It happens in a few steps:

- Prognostic models are fit on prior year's data, resulting in outcome models.
- Outcome models are used to predict prognostic scores and calculate a caliper
- For each pair of treatment and control schools, we do a school-by-school calculation:
  - Calculate a "bias" score reflecting the closeness of the two schools' prognostic scores
  - Calculate an "effective sample size" score reflecting the effective sample size that would come from a match of these two schools
- We take the geometric mean of these two scores to return the final matchAhead distance matrix

The method only takes a single researcher-supplied parameter: the largest permissible size of a student-level match. This procedure will be contrasted with the Pimentel procedure.